Claims

1. A method of removing a part of a transgene after its integration into a genome comprising flanking said part of the transgene on each side thereof with an attachment P region (attP) of bacteriophage λ, the attP region comprises a nucleic acid sequence as set forth in SEQ ID NO:1 or fragment thereof which maintains the same function, or nucleic acids which hybridise under stringent conditions to the DNA of SEQ ID NO:1 and function as an attP region, or nucleic acids which differ from the DNA of SEQ ID NO:1 due to the degeneracy of the genetic code and which function as an attP region, and inducing a high frequency of intrachromasomal homologous recombination between flanking attP regions whereby said part of the transgene sandwiched therebetween is removed.

2. A method as claimed in Claim 1 characterised in that said transgene comprises a marker gene and/or vector sequence and/or other foreign ancillary nucleic acid.

3. A method as claimed in Claim 1 or Claim 2 characterised in that the marker gene confers resistance to antibiotics and/or herbicide resistance.

4. A method as claimed in any one of the preceding claims characterised in that the marker gene is involved in specific biosynthetic pathways and/or involved in environmental tolerance.

5. A method as claimed in any one of the preceding claims characterised in that the marker gene is selected from the group consisting of *nptII*, Ble, *dhfr*, *cat*, *aphIV*, SPT, *aaaC3*, *aaaC4*, *bar*, EPSP, *bxn*, *psbA*, *tfdA*, DHPS, AK, *sul*, *crs1-1* and *tdc*.

6. A method as claimed in any one of the preceding claims characterised in that more than one marker gene and/or vector sequence and/or foreign nucleic acid part is

removed from the transgene and each such part is to be removed is flanked by an attP region.

7. A method as claimed in any one of the preceding claims characterised in that the attP region comprises 352 basepairs, or functionally equivalent fragment thereof, located between positions 27492 and 27844 of bacteriophage λ.

8. A method as claimed in any one of the preceding claims characterised in that the attP regions are in a cassette.

9. A method as claimed in Claim 8 characterised in that the cassette further includes a transformation booster sequence or fragment thereof for enhancing homologous and illegitimate recombination.

10. A method as claimed in Claim 8 or Claim 9 characterised in that the cassette includes an effector gene such as oryzacyctastin-I or functional equivalent thereof.

11. A method as claimed in any one of the preceding claims characterised in that the genome is a plant genome.

12. A plant or plant cell or plant tissue whenever produced by the method of any one of Claims 1 to 11.

13. A method which comprises performing the method of Claim 11 to produce a plant or providing a plant or plant cell or plant tissue of Claim 12 and, in either case growing the plant and/or harvesting products therefrom.

14. A plant or plant cell or plant tissue comprising recombinant attP regions.

15. An attP recombination cassette comprising a marker gene and/or vector sequence and/or foreign ancillary nucleic acid flanked on either side by an attP region

the attP region comprising a nucleic acid sequence as set forth in SEQ ID NO:1 or fragment thereof which maintains the same function, or nucleic acids which hybridise under stringent conditions to the DNA of SEQ ID NO:1 and function as an attP region, or nucleic acids which differ from the DNA of SEQ ID NO:1 due to the degeneracy of the genetic code and which function as an attP region.

16. Use of an attP recombination cassette of Claim 15 for removing a part integrated into a plant genome.

17. A kit for removing a part of a transgene after its integration into a plant genome comprising an attP recombination cassette as claimed in Claim 15.

18. A plant or plant cell or plant tissue comprising a recombinant transgene integrated into its genome characterised in that the transgene is associated with a bacteriophage λ attP region on respective sides thereof, the attP region comprising a nucleic acid sequence as set forth in SEQ ID NO:1 or fragment thereof which maintains the same function, or nucleic acids which hybridise under stringent conditions to the DNA of SEQ ID NO:1 and function as an attP region, or nucleic acids which differ from the DNA of SEQ ID NO:1 due to the degeneracy of the genetic code and which function as an attP region.

19. A plant or plant cell or plant tissue as claimed in Claim 18 characterised in that it includes one such bacteriophage λ attP region and one effector transgene integrated into its genome.

20. A plant or plant cell or plant tissue as claimed in Claim 19 characterised in that the bacteriophage λ attP regions and one transgene are not associated with a marker gene and/or vector sequence and/or other foreign ancillary nucleic acid.

21. A plant or plant cell or plant tissue as claimed in any one of Claims 18 to 20 characterised in that the transgene is further associated with a transformation booster

sequence or fragment thereof which is capable of enhancing homologous and illegitimate recombination.

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